RAW SEQUENCE LISTING   DATE: 01/28/2002
PATENT APPLICATION: US/10/007,262   TIME: 11:37:02

Input Set : N:\Crf3\RULE60\10007262.raw
Output Set: N:\CRF3\01282002\J007262.raw

```
 1 <110> APPLICANT: Bistrup, Annette
 2         Rosen, Steven D.
 3         Tangemann, Kirsten
 4         Hemmerich, Stefan
 5 <120> TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
 6 <130> FILE REFERENCE: 6510-107CIP
 7 <140> CURRENT APPLICATION NUMBER: 10/007,262
 8 <141> CURRENT FILING DATE: 2001-11-08
 9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/190,911
W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12
11 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 386
16 <212> TYPE: PRT
17 <213> ORGANISM: H. sapiens
18 <400> SEQUENCE: 1
19      Met Leu Leu Pro Lys Lys Met Lys Leu Leu Leu Phe Leu Val Ser Gln
20       1           5                   10                  15
21      Met Ala Ile Leu Ala Leu Phe Phe His Met Tyr Ser His Asn Ile Ser
22                   20                  25                  30
23      Ser Leu Ser Met Lys Ala Gln Pro Glu Arg Met His Val Leu Val Leu
24               35                  40                  45
25      Ser Ser Trp Arg Ser Gly Ser Ser Phe Val Gly Gln Leu Phe Gly Gln
26           50                  55                  60
27      His Pro Asp Val Phe Tyr Leu Met Glu Pro Ala Trp His Val Trp Met
28      65                  70                  75                  80
29      Thr Phe Lys Gln Ser Thr Ala Trp Met Leu His Met Ala Val Arg Asp
30                       85                  90                  95
31      Leu Ile Arg Ala Val Phe Leu Cys Asp Met Ser Val Phe Asp Ala Tyr
32                   100                 105                 110
33      Met Glu Pro Gly Pro Arg Arg Gln Ser Ser Leu Phe Gln Trp Glu Asn
34               115                 120                 125
35      Ser Arg Ala Leu Cys Ser Ala Pro Ala Cys Asp Ile Ile Pro Gln Asp
36           130                 135                 140
37      Glu Ile Ile Pro Arg Ala His Cys Arg Leu Leu Cys Ser Gln Gln Pro
38      145                 150                 155                 160
39      Phe Glu Val Val Glu Lys Ala Cys Arg Ser Tyr Ser His Val Val Leu
40                       165                 170                 175
41      Lys Glu Val Arg Phe Phe Asn Leu Gln Ser Leu Tyr Pro Leu Leu Lys
42                   180                 185                 190
43      Asp Pro Ser Leu Asn Leu His Ile Val His Leu Val Arg Asp Pro Arg
44               195                 200                 205
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45        Ala Val Phe Arg Ser Arg Glu Arg Thr Lys Gly Asp Leu Met Ile Asp
46            210             215             220
47        Ser Arg Ile Val Met Gly Gln His Glu Gln Lys Leu Lys Lys Glu Asp
48        225             230             235             240
49        Gln Pro Tyr Tyr Val Met Gln Val Ile Cys Gln Ser Gln Leu Glu Ile
50                        245             250             255
51        Tyr Lys Thr Ile Gln Ser Leu Pro Lys Ala Leu Gln Glu Arg Tyr Leu
52                    260             265             270
53        Leu Val Arg Tyr Glu Asp Leu Ala Arg Ala Pro Val Ala Gln Thr Ser
54            275             280             285
55        Arg Met Tyr Glu Phe Val Gly Leu Glu Phe Leu Pro His Leu Gln Thr
56            290             295             300
57        Trp Val His Asn Ile Thr Arg Gly Lys Gly Met Gly Asp His Ala Phe
58        305             310             315             320
59        His Thr Asn Ala Arg Asp Ala Leu Asn Val Ser Gln Ala Trp Arg Trp
60                        325             330             335
61        Ser Leu Pro Tyr Glu Lys Val Ser Arg Leu Gln Lys Ala Cys Gly Asp
62                    340             345             350
63        Ala Met Asn Leu Leu Gly Tyr Arg His Val Arg Ser Glu Gln Glu Gln
64            355             360             365
65        Arg Asn Leu Leu Leu Asp Leu Leu Ser Thr Trp Thr Val Pro Glu Gln
66            370             375             380
67        Ile His
68        385
70  <210> SEQ ID NO: 2
71  <211> LENGTH: 2032
72  <212> TYPE: DNA
73  <213> ORGANISM: H. sapiens
74  <400> SEQUENCE: 2
75        ggctcgaggc caggatgcct ccagtctggg ggaaaatgct tcctcatttg cttctcccag      60
76        cccacctcaa gcagtctccc cacccttga gtctcagcag tgttaaagct gttactttca      120
77        cagcttcctg ggagcgagtg ctttctcaag cccgtcttgc aaggtcttcc acttcagcac      180
78        aatgctactg cctaaaaaaa tgaagctcct gctgtttctg gtttcccaga tggccatctt      240
79        ggctctattc ttccacatgt acagccacaa catcagctcc ctgtctatga aggcacagcc      300
80        cgagcgcatg cacgtgctgg ttctgtcttc ctggcgctct ggctcttctt ttgtggggca      360
81        gcttttgggg cagcacccag atgttttcta cctgatggag cccgcctggc acgtgtggat      420
82        gaccttcaag cagagcaccg cctggatgct gcacatggct gtgcgggatc tgatacgggc      480
83        cgtcttcttg tgcgacatga gcgtctttga tgcctacatg gaacctggtc cccggagaca      540
84        gtccagcctc tttcagtggg agaacagccg ggccctgtgt tctgcacctg cctgtgacat      600
85        catcccacaa gatgaaatca tcccccgggc tcactgcagg ctcctgtgca gtcaacagcc      660
86        ctttgaggtg gtggagaagg cctgccgctc ctacagccac gtggtgctca aggaggtgcg      720
87        cttcttcaac ctgcagtccc tctacccgct gctgaaagac ccctccctca acctgcatat      780
88        cgtgcacctg gtccgggacc cccgggccgt gttccgttcc cgagaacgca caaagggaga      840
89        tctcatgatt gacagtcgca ttgtgatggg gcagcatgag cagaaactca gaaggagga      900
90        ccaaccctac tatgtgatgc aggtcatctg ccaaagccag ctggagatct acaagaccat      960
91        ccagtccttg cccaaggccc tgcaggaacg ctacctgctt gtgcgctatg aggacctggc      1020
92        tcgagcccct gtggcccaga cttcccgaat gtatgaattc gtgggattgg aattcttgcc      1080
93        ccatcttcag acctgggtgc ataacatcac ccgaggcaag ggcatgggtg accacgcttt      1140
94        ccacacaaat gccagggatg cccttaatgt ctcccaggct ggcgctggt ctttgcccta      1200
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 95        tgaaaaggtt tctcgacttc agaaagcctg tggcgatgcc atgaatttgc tgggctaccg    1260
 96        ccacgtcaga tctgaacaag aacagagaaa cctgttgctg gatcttctgt ctacctggac    1320
 97        tgtccctgag caaatccact aagaggggttg agaaggcttt gctgccacct ggtgtcagcc    1380
 98        tcagtcactt tctctgaatg cttctgagcc ttgcctacat ctctgagcct taactacatg    1440
 99        tctgtgggta tcacactgag tgtgagttgt gtccacacgt gctcaagcag aaggactttt    1500
100        gtgtccatgc ttgtgtctag aaaacagact ggggaacctt atgtgagcag cacatcccac    1560
101        cagtgaaaca gggtattgct cttcttcttt tcttgatctt cctgtctggg cagacttcag    1620
102        agactttgtg gcctggaggc ctattaagca cgacacagta tcagtggaat tgatccataa    1680
103        acctccctgt ccacatcttg cccaatgggg aatggatctt tcaccaaaga gctcaccagc    1740
104        attttccaca gagatgcaaa ttctgagccc ttggagttcc cagtggattc aaggaaggaa    1800
105        gtgggaacaa ggttggatgc ctacttatga gcttgaccat cacagctatc ggtaatcaga    1860
106        aatatgaaac aaaatctctg cacaaaagag caagctctta agttcacagg gtgcctgggc    1920
107        tgcatttgaa tatcacttcc cctctgcatt ttcccatcac atagaagact ttgacctgtg    1980
108        aagctgccat ctgttaatac taaaattccc aaataagaaa aaaaaaaaa aa             2032
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 29
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: primer
116 <220> FEATURE:
117 <221> NAME/KEY: misc_feature
118 <222> LOCATION: (1)...(29)
119 <223> OTHER INFORMATION: n = inosine
120 <400> SEQUENCE: 3
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W--> 121   twytwyctnt wygarccnct ntggcayst   29

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123 <210> SEQ ID NO: 4
124 <211> LENGTH: 29
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: primer
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (1)...(29)
132 <223> OTHER INFORMATION: n = inosine
133 <400> SEQUENCE: 4
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W--> 134   ctnaanctns tncwrctnst nmgnraycc   29

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136 <210> SEQ ID NO: 5
137 <211> LENGTH: 29
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
140 <220> FEATURE:
141 <223> OTHER INFORMATION: primer
142 <220> FEATURE:
143 <221> NAME/KEY: misc_feature
144 <222> LOCATION: (1)...(29)
145 <223> OTHER INFORMATION: n = inosine
146 <400> SEQUENCE: 5
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RAW SEQUENCE LISTING                    DATE: 01/28/2002
PATENT APPLICATION:  US/10/007,262      TIME: 11:37:02

         Input Set : N:\Crf3\RULE60\10007262.raw
         Output Set: N:\CRF3\01282002\J007262.raw
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W--> 147        ggrtynckna snagywgnas nagnttnag                    29
     149 <210> SEQ ID NO: 6
     150 <211> LENGTH: 26
     151 <212> TYPE: DNA
     152 <213> ORGANISM: Artificial Sequence
     153 <220> FEATURE:
     154 <223> OTHER INFORMATION: primer
     155 <220> FEATURE:
     156 <221> NAME/KEY: misc_feature
     157 <222> LOCATION: (1)...(26)
     158 <223> OTHER INFORMATION: n = inosine
     159 <400> SEQUENCE: 6
W--> 160        agrtcytcrt ancknagnag nakrta                       26
     162 <210> SEQ ID NO: 7
     163 <211> LENGTH: 37
     164 <212> TYPE: DNA
     165 <213> ORGANISM: H. sapiens
     166 <400> SEQUENCE: 7
     167        aaactcaaga aggaggacca accctactat gtgatgc           37
     169 <210> SEQ ID NO: 8
     170 <211> LENGTH: 47
     171 <212> TYPE: DNA
     172 <213> ORGANISM: H. sapiens
     173 <400> SEQUENCE: 8
     174        ataaagcttg tggatttgtt cagggacatt ccaggtagac agaagat  47
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VERIFICATION SUMMARY   DATE: 01/28/2002
PATENT APPLICATION: US/10/007,262   TIME: 11:37:03

Input Set : **N:\Crf3\RULE60\10007262.raw**
Output Set: **N:\CRF3\01282002\J007262.raw**

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L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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